

Abstract

A method is described for the identification of 5-methylcytosine positions in genomic DNA, which is characterized by the fact that the following method steps are conducted:

- a) the genomic DNA of a cell, a cell line, a tissue, or an individual is chemically treated in such a way that cytosine and 5-methylcytosine react differently and a different base pairing behavior of the two products is produced in the duplex,
- b) the same nucleic-acid segment is amplified by means of a polymerase reaction,
- c) the same nucleic-acid segment of at least one other cell, cell line, tissue or individual or any reference DNA is treated according to items a) and b),
- d) heteroduplexes are formed from the at-least two amplified products of items b) and c),
- e) a label that can be displayed is introduced into the heteroduplex by a reaction, which is specific for non-complementary base pairs.

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